Supplementary Information

"Cortisol overproduction results from DNA methylation of CYP11B1 in hypercortisolemia"

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Table S1. Characteristics of Patients with Cortisol-Producing Adenomas

| Case | Age/ Gender | Cushingoid signs | BMI | HT | DM/ IGT | HL | ACTH (pg/mL) | F (nmol/L) | 24h urinary F (μg/day) | Midnight F (nmol/L) | 1mg DST-F (nmol/L) | Tumor size (mm) | Gene Mutation |
|------|----------------|---------------------|------|-----|------------|-----|-----------------|---------------|---------------------------|---------------------------|--------------------------|-----------------------|------------------|
| 1 | 44/F | (-) | 19.3 | (+) | (-) | (-) | 6 | 322 | ND | ND | 226 | 19 | PRKACA p.L206R |
| 2 | 37/F | (+) | 27.1 | (+) | (+) | (+) | <5 | 348 | 93 | 372 | 361 | 25 | PRKACA p.L206R |
| 3 | 60/F | (-) | 22.1 | (+) | (-) | (+) | 11 | 436 | 42 | 119 | 155 | 24 | GNAS p.R201H |
| 4 | 64/M | (-) | 23.7 | (+) | (+) | (-) | <5 | 441 | 75 | 149 | 166 | 30 | GNAS p.R201H |
| 5 | 44/F | (-) | 18.4 | (+) | (-) | (-) | 17 | 521 | 36 | 127 | 279 | 20 | GNAS p.R201H |
| 6 | 58/F | (-) | 20.4 | (+) | (-) | (-) | <5 | 212 | 35 | 348 | 102 | 13 | GNAS p.R201S |
| 7 | 52/M | (+) | 32.5 | (+) | (-) | (-) | 11 | 480 | 136 | 530 | 571 | 27 | GNAS p.R201C |
| 8 | 58/F | (-) | 26.6 | (+) | (-) | (-) | 6 | 223 | 31 | 138 | 135 | 22 | GNAS p.Q227R |
| 9 | 61/F | (-) | 20.7 | (+) | (-) | (-) | <5 | 430 | 44 | 160 | 83 | 30 | WT |
| 10 | 33/F | (-) | 29.6 | (+) | (-) | (-) | <5 | 221 | 31 | 243 | 259 | 23 | WT |
| 11 | 55/M | (-) | 21.1 | (-) | (-) | (-) | 16 | 428 | 40 | 179 | 83 | 30 | WT |
| 12 | 53/F | (-) | 22.1 | (+) | (+) | (-) | <5 | 417 | 70 | 579 | 643 | 23 | WT |
| 13 | 65/M | (-) | 30.5 | (+) | (-) | (+) | 5 | 221 | ND | ND | 69 | 45 | WT |

BMI, body mass index; HT, hypertension; DM, diabetes mellitus; IGT, impaired glucose tolerance; HL, hyperlipidemia; F, serum cortisol concentration; DST, dexamethasone suppression test; ND, no data; WT, wild type for both *PRKACA* and *GNAS* genes. '(+)' represents positive, and '(-)' represents negative.

Table S2. Characteristics of Patients with Non-Functioning Adrenal Tumor

| Case | Age/ Gender | Cushingoid signs | BMI | HT | DM/ IGT | HL | ACTH (pg/mL) | F (µg/dL) | 24h urinary F (µg/day) | Midnight F (µg/dL) | 1mg DST-F (µg/dL) | Tumor size (mm) | Final Diagnosis |
|------|----------------|---------------------|------|-----|------------|-----|-----------------|--------------|---------------------------|-----------------------|-------------------------|-----------------------|-----------------|
| 14 | 61/F | (-) | 20.2 | (-) | (-) | (-) | 23 | 11 | 14 | 4 | 1 | 11 | NFT |
| 15 | 57/F | (-) | 21.4 | (-) | (-) | (-) | 25 | 15 | 35 | 2 | 1 | 32 | NFT |
| 16 | 40/M | (-) | 22.0 | (-) | (-) | (-) | 10 | 12 | ND | ND | 1 | 28 | NFT |
| 17 | 24/M | (-) | 18.8 | (-) | (-) | (-) | 29 | 14 | 31 | 5 | 1 | 45 | NFT |
| 18 | 78/F | (-) | 22.4 | (-) | (-) | (-) | 8 | 14 | 37 | 6 | 1 | 37 | NFT |
| 19 | 62/M | (-) | 32.5 | (+) | (-) | (+) | 11 | 11 | 60 | 5 | 1 | 21 | NFT |
| 20 | 44/F | (-) | 19.7 | (-) | (-) | (-) | 24 | 6 | 64 | 2 | 0.2 | 160 | NFT |

NFT, non-functioning adrenal tumor; BMI, body mass index; HT, hypertension; DM, diabetes mellitus; IGT, impaired glucose tolerance; HL, hyperlipidemia; F, serum cortisol concentration; DST, dexamethasone suppression test; ND, no data. '(+)' represents positive, and '(-)' represents negative.

Table S3. Primers used for pyrosequencing

| Primer | Sequence (5' to 3') |
|--------------------|--------------------------------|
| CYP11B1 Pyro-F 1-2 | TTGTAATTTTTATTTTGTTTGGTGTTT |
| CYP11B1 Pyro-R 1-2 | ATACACCCCAATAAATCCCTAC |
| CYP11B1 Pyro-S1 | TGTTTGGTGTTTT |
| CYP11B1 Pyro-S2 | TGGTTTTGGATTTGTTTGAG |
| CYP11B1 Pyro-F3 | AGGTTAGGGTTGGAGGTAGG |
| CYP11B1 Pyro-R3 | AACCCCATCCATCTTACTCCTC |
| CYP11B1 Pyro-S3 | ATTGGGGGTGTATGA |
| CYP11B1 Pyro-F4 | GGATGGGGTTTTTATTTTATTTAAGAGT |
| CYP11B1 Pyro-R4 | CCCAATAATCATTCAAAAACAAATTACTCA |
| CYP11B1 Pyro-S4 | ATTTATTTTTTGTAAGGTTTATA |

^{&#}x27;F', 'R' and 'S' indicate forward, reverse and sequence primers, respectively. The 5' ends of reverse primers are biotinylated.

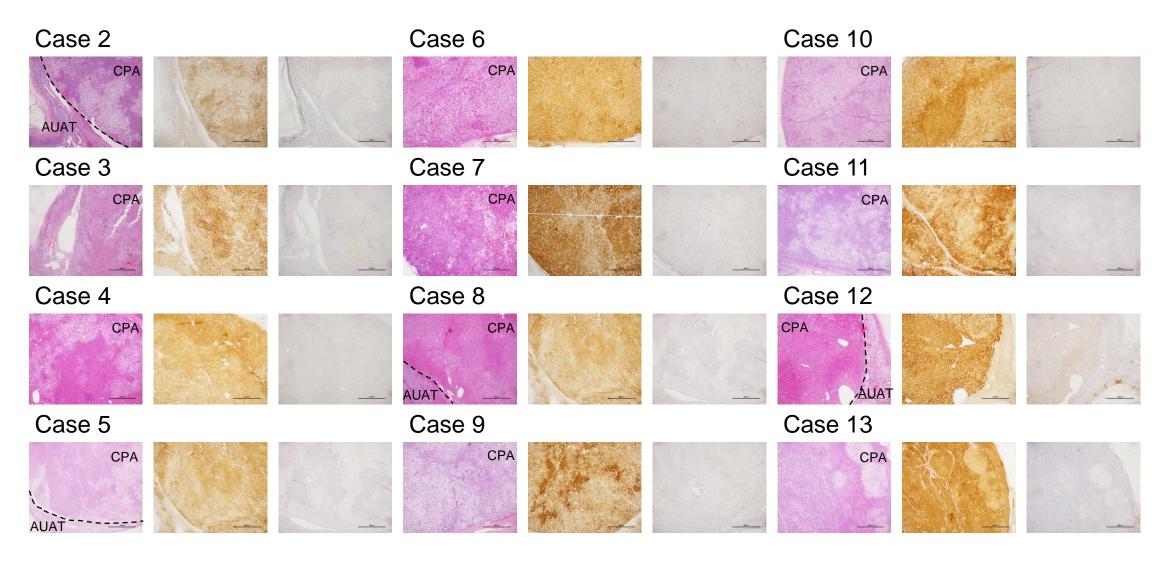


Figure S1. Immunohistochemical analysis of *CYP11B1* overexpression in all cases of cortisol-producing adenomas

Formalin-fixed paraffin-embedded tissue sections were stained with Hematoxylin & Eosin (HE) (left), anti-CYP11B1 (middle), and anti-CYP11B2 antibodies (right). CPA, cortisol-producing adenoma; AUAT, adjacent unaffected adrenal tissue.

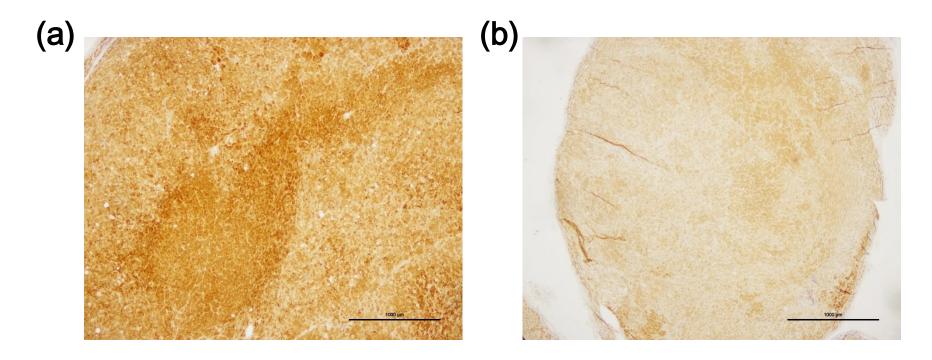


Figure S2. Two cortisol-producing adenomas with atypical CYP11B1 staining patterns (case 10) **a**, The tumor with stronger staining. **b**, The tumor with weaker staining.

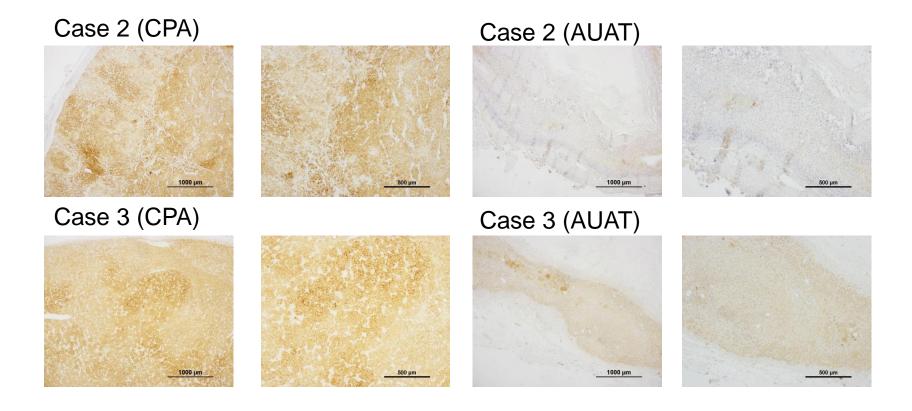


Figure S3. Immunohistochemical analysis of *CYP11B1* expression in cortisol-producing adenomas and adjacent unaffected adrenal tissue

Formalin-fixed paraffin-embedded tissue sections were stained with anti-CYP11B1. *CYP11B1* expression in CPAs was higher than AUATs in both cases.

CPA, cortisol-producing adenoma; AUAT, adjacent unaffected adrenal tissue.

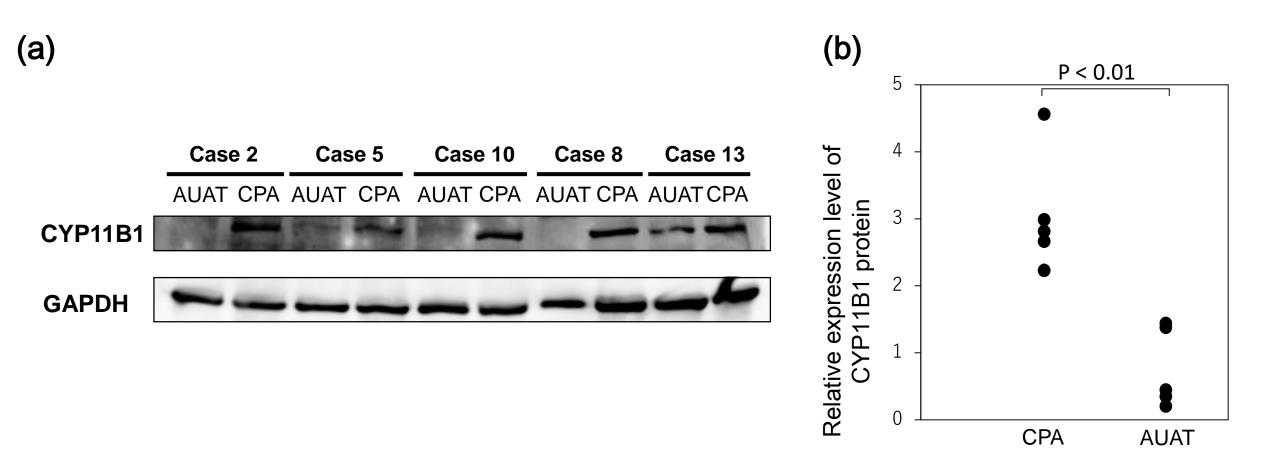
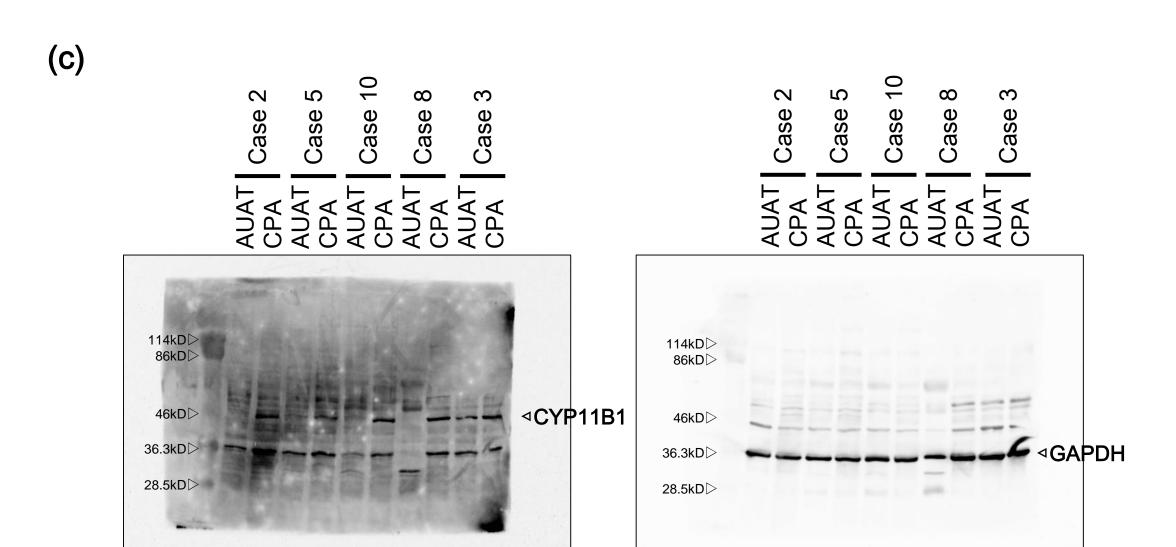


Figure S4. Expression of CYP11B1 protein in cortisol-producing adenoma

a, Western blot analysis of tissue homogenates (20 µg of protein) by using anti-CYP11B1 and anti-GAPDH antibodies. Full-length blots are shown in Figure S4c.

AUAT, adjacent unaffected adrenal tissue; CPA, cortisol-producing adenoma.

b, The density of each band was measured by LAS-1000 image analyzer, and data were normalized to GAPDH. The x-axis represents the tissue sample category: CPA (n = 5) and AUAT (n = 5). The mean of AUAT was set to 1.0. Significant difference was evaluated by the Mann-Whitney U test.



CYP11B1 GAPDH

Figure S4. Expression of CYP11B1 protein in cortisol-producing adenoma c, Full-length blots of CYP11B1 (left panel) and GAPDH (right panel) are shown.

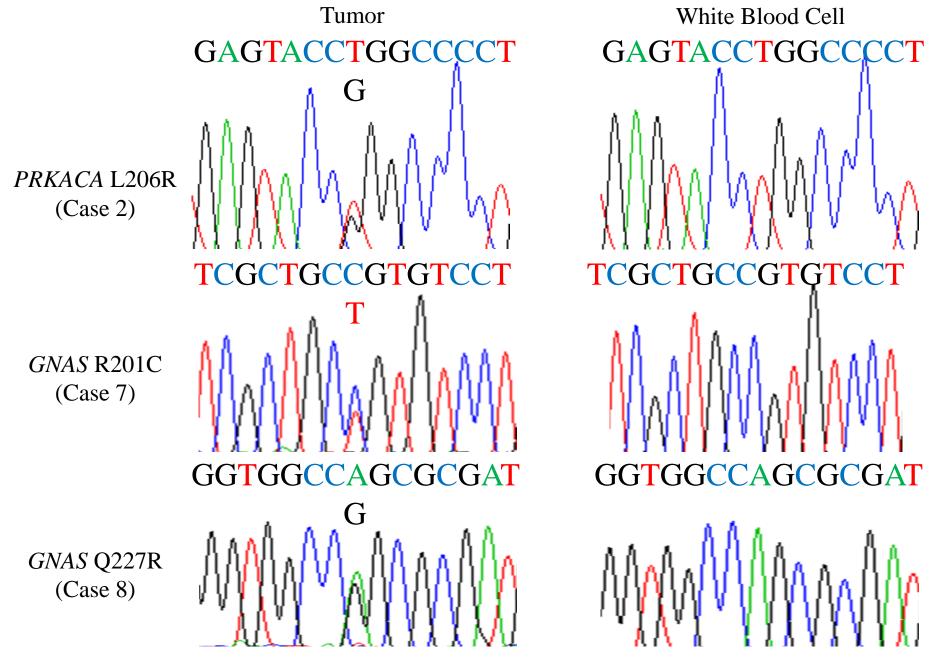
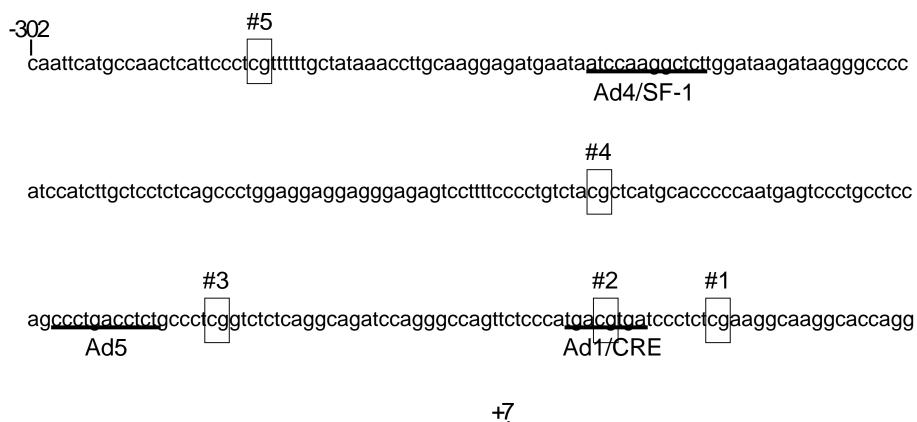


Figure S5. Gene mutation analysis of PRKACA and GNAS gene



caagataaaaggattgcagctgaacagggtggagggagcattggaATGGCA...

Figure S6. Oligonucleotide sequence of the DNA fragment spanning -302 (relative to the transcription start site) to +7 of the human *CYP11B1* gene

Transcription factor-binding sites are indicated with underlines, and each open square represents one CpG site. Note that the start codon of CYP11B1 is located at +8 to +10.

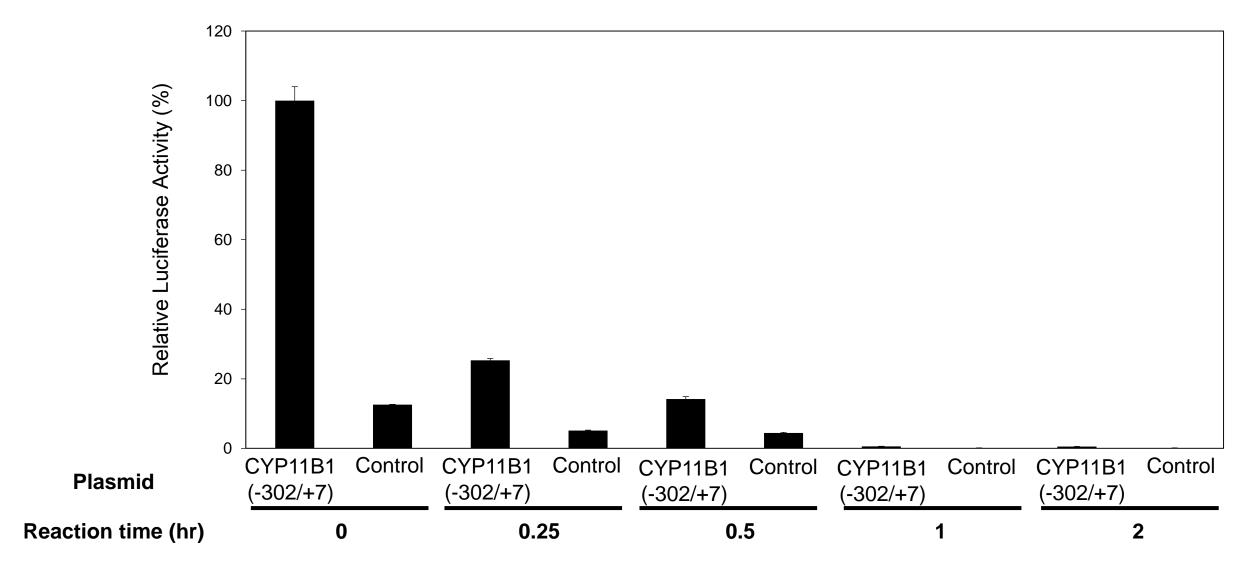


Figure S7. Effect of methylation on luciferase activity of reporter plasmids Both pGL4.10[luc2](control) and pGL4-cyp11b1[-302/+7](CYP11B1[-302/+7]) were incubated with the CpG methyltransferase M.Sssl for the indicated period and subject to Luciferase assay. Note here that although the luciferase activity of the control plasmid was reduced by methylation, the effect of methylation was smaller when compared with pGL4-cyp11b1[-302/+7]. Luciferase activity of the unmethylated CYP11B1[-302/+7]) sample (reaction time = 0 h) was set to 100%, and the mean \pm SEM (n = 4) of the data are shown.

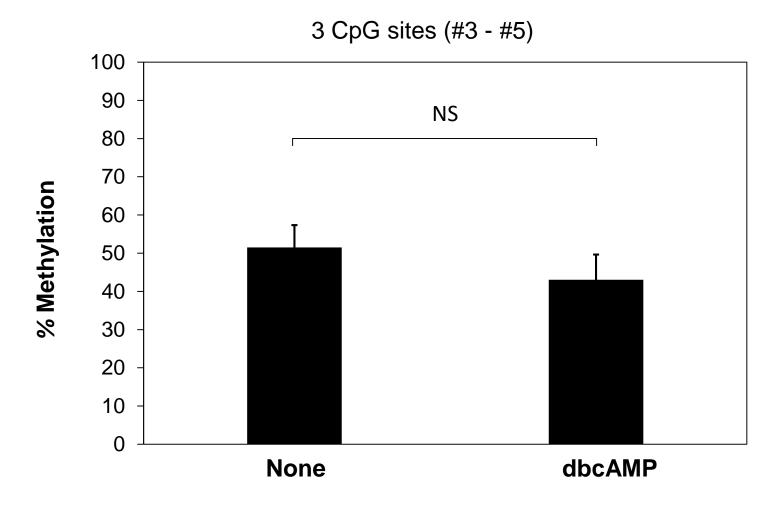


Figure S8. Effect of dbcAMP treatment on DNA methylation at CpG#3-5 of the CYP11B1 promoter After stimulation with dbcAMP, methylation levels at 3 CpG sites (#3 - #5) in the CYP11B1 promoter was measured by pyrosequencing. Data are shown as the mean \pm SEM (n=3), and analyzed by the Mann-Whitney U test.

NS, not significant.

DNA marker

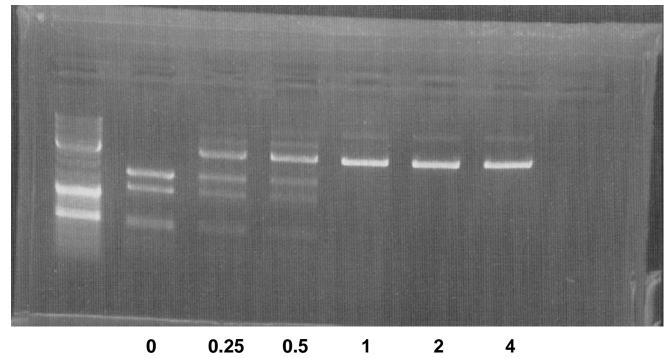


Figure S9. Confirmation of plasmid methylation Full-length gel of Figure 4b is shown.

Reaction time (hr)